

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2000, 22:23:27 ; Search time 2981.65 Seconds  
(without alignments)  
172.089 Million cell updates/sec

Title: PCT-US99-26055-10

Perfect score: 120  
Sequence: 1 gtgaacagaggagggaag.....tgagccacaccttcacatg 120

Scoring table: OLIGO\_NUC

Searched: 780561 seqs, 2137953050 residues

Database : GenEmbl.\*

- 1: gb\_bal.\*
- 2: gb\_ba2.\*
- 3: gb\_om.\*
- 4: gb\_ov.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
- 9: gb\_pl1.\*
- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sts.\*
- 14: gb\_sy.\*
- 15: gb\_un.\*
- 16: gb\_v1.\*
- 17: gb\_v2.\*
- 18: gb\_v3.\*
- 19: gb\_v4.\*
- 20: gb\_v5.\*
- 21: gb\_v6.\*
- 22: gb\_v7.\*
- 23: gb\_v8.\*
- 24: gb\_v9.\*
- 25: gb\_v10.\*
- 26: gb\_v11.\*
- 27: gb\_v12.\*
- 28: gb\_v13.\*
- 29: gb\_v14.\*
- 30: gb\_v15.\*
- 31: gb\_v16.\*
- 32: gb\_v17.\*
- 33: gb\_v18.\*
- 34: gb\_v19.\*
- 35: gb\_v20.\*
- 36: gb\_v21.\*
- 37: gb\_v22.\*
- 38: gb\_v23.\*
- 39: gb\_v24.\*
- 40: gb\_v25.\*
- 41: gb\_v26.\*
- 42: gb\_v27.\*
- 43: gb\_v28.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
------------	-------	-------	-------	--------	----	----	-------------

1	120	100.0	118788	11	AC005277	11	AC005277	AC005277 Homo sapi
2	23	19.2	43514	11	AC005545	11	AC005545	AC005545 Homo sapi
3	18	15.0	177568	10	HS388M5	10	HS388M5	297055 Human DNA s
4	18	15.0	12518	11	HS00C202	11	HS00C202	U41111 Human mitog
5	18	15.0	175093	33	CNS01DRF	33	CNS01DRF	AL111790 Homo sapi
6	18	15.0	226345	41	AC005406	41	AC005406	AC005406 , complet
7	18	15.0	117639	41	AC005866	41	AC005866	AC005866 Homo sapi
8	17	14.2	10176	3	AF005497	3	AF005497	AF005497 Bos tauru
9	17	14.2	2200	4	DR054796	4	DR054796	U54796 Danio rerio
10	17	14.2	163795	9	AP000356	9	AP000356	AP000356 Homo sapi
11	17	14.2	147135	9	HS368A4	9	HS368A4	283843 Human DNA s
12	17	14.2	39756	9	HS111386	9	HS111386	269837 Human DNA s
13	17	14.2	28031	9	HS111386	9	HS111386	284495 Human DNA s
14	17	14.2	1542	9	HUMD123A	9	HUMD123A	DL4878 Human mRNA
15	17	14.2	69017	10	HS41018	10	HS41018	AL031732 Human DNA
16	17	14.2	143453	10	HS7661G12	10	HS7661G12	AL049797 Human DNA
17	17	14.2	200348	11	AC005516	11	AC005516	AC005516 Homo sapi
18	17	14.2	147902	11	AC005670	11	AC005670	AD005670 Homo sapi
19	17	14.2	110096	11	CH19HR23	11	CH19HR23	AD000092 Homo sapi
20	17	14.2	3655	11	HS090094	11	HS090094	U90094 Human chrom
21	17	14.2	1371	11	U27112	11	U27112	U27112 Homo sapien
22	17	14.2	36534	11	U73167	11	U73167	U73167 Homo sapien
23	17	14.2	67977	12	AB010266	12	AB010266	AB010266 Mus muscu
24	17	14.2	119865	12	AC004407	12	AC004407	AC004407 Mus muscu
25	17	14.2	13297	12	AC005835	12	AC005835	AC005835 Mus muscu
26	17	14.2	591	12	AF032459	12	AF032459	AF032459 Mus muscu
27	17	14.2	423	12	AF032460	12	AF032460	AF032460 Mus muscu
28	17	14.2	333	12	AF032461	12	AF032461	AF032461 Mus muscu
29	17	14.2	333	12	AF065432	12	AF065432	AF065432 Rattus no
30	17	14.2	591	12	AF065433	12	AF065433	AF065433 Rattus no
31	17	14.2	423	12	AF136927	12	AF136927	AF136927 Rattus no
32	17	14.2	6708	12	MUSCICLORA	12	MUSCICLORA	L04289 Mouse cyclo
33	17	14.2	353	13	G25238	13	G25238	G25238 human STS E
34	17	14.2	395	13	G29573	13	G29573	G29573 human STS S
35	17	14.2	1557	25	E11207	25	E11207	E11207 Human CDNA
36	17	14.2	119000	33	AC003656_3	33	AC003656_3	Continuation (4 of
37	17	14.2	56078	33	HSJ9817	33	HSJ9817	AJ009617 Homo sapi
38	17	14.2	106606	33	HSJ9817	33	HSJ9817	AL078461 Homo sapi
39	17	14.2	74780	34	AC005445	34	AC005445	AC005445 Drosophil
40	17	14.2	166214	34	AC006735	34	AC006735	AC006735 Caenorhab
41	17	14.2	86408	34	AC007952	34	AC007952	AC007952 Homo sapi
42	17	14.2	27396	35	CELC54G6	35	CELC54G6	AF043698 Caenorhab
43	17	14.2	686	35	LM5KDINS	35	LM5KDINS	X17024 Locusta mig
44	17	14.2	528	35	LMGIRP3	35	LMGIRP3	Z29964 L.migratori
45	17	14.2	159821	41	AC009743	41	AC009743	AC009743 Homo sapi

ALIGNMENTS

RESULT	1	AC005277	118788 bp	DNA	PRI	23-JUL-1998
LOCUS		AC005277				
DEFINITION		Homc sapiens chromosome 17, clone hRPK.597_M.12, complete sequence.				
ACCESSION		AC005277				
NID		93337311				
VERSION		AC005277.1				
KEYWORDS		HTG.				
SOURCE		Human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
THORS		Eutheria; Primates; Catarrhini; Hominidae; Homo.				
FILE		1 (bases 1 to 118788)				
JOURNAL		Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,				
REFERENCE		2 (bases 1 to 118788)				
THORS		Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,				
FILE		Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatman,C.,				
JOURNAL		Boutwell,C., Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E.,				
REFERENCE		Devon,K., Dewar,K., Donelan,L., Etemadi,S., Ferreira,P.,				
THORS		Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Gardyna,S.,				
FILE		Gensheimer,S., Geraigery,K., Gilmartin,T., Grant,G., Hagos,B.,				

Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Melchior, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J., and Zody, M.

Direct Submission  
Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 118788)

REFERENCE  
AUTHORS  
Birken, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Castile, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donellan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Grainger, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Melchior, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J., and Zody, M.

TITLE  
JOURNAL  
Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT  
On Jul 23, 1998 this sequence version replaced gi:3335015.  
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Only the first 118.8 kilobases of this clone are being submitted.  
The remainder overlaps accession number AC005274 (WICGR project L350).

FEATURES	source	Location/Qualifiers
repeat_region	repeat_region	1..118788
repeat_region	repeat_region	/organism="Homo sapiens"
repeat_region	repeat_region	/db_xref="taxon:9606"
repeat_region	repeat_region	/clone="hAPK 597 M_12"
repeat_region	repeat_region	/clone_lib="RPC1-11 human BAC library"
repeat_region	repeat_region	/map="17"
repeat_region	repeat_region	/chromosome="17"
repeat_region	repeat_region	795..884
repeat_region	repeat_region	/rpt_family="MIR"
repeat_region	repeat_region	complement(932..1000)
repeat_region	repeat_region	/rpt_family="MIR"
repeat_region	repeat_region	2044..2076
repeat_region	repeat_region	/rpt_family="AT_rich"
repeat_region	repeat_region	2237..2713
repeat_region	repeat_region	/rpt_family="MER34"
repeat_region	repeat_region	2718..3477
repeat_region	repeat_region	/rpt_family="L2"
repeat_region	repeat_region	complement(3478..3821)
repeat_region	repeat_region	/rpt_family="MLT1A"
repeat_region	repeat_region	3822..4007
repeat_region	repeat_region	/rpt_family="L2"
repeat_region	repeat_region	complement(4015..4281)
repeat_region	repeat_region	/rpt_family="MER89"
repeat_region	repeat_region	complement(4282..4321)
repeat_region	repeat_region	/rpt_family="(TAAA)n"
repeat_region	repeat_region	complement(4328..4608)
repeat_region	repeat_region	/rpt_family="AluSx"
repeat_region	repeat_region	complement(4609..4895)
repeat_region	repeat_region	/rpt_family="MER89"
repeat_region	repeat_region	complement(4896..5186)
repeat_region	repeat_region	/rpt_family="AluSp"
repeat_region	repeat_region	5219..5479
repeat_region	repeat_region	/rpt_family="L2"
repeat_region	repeat_region	complement(5481..5740)
repeat_region	repeat_region	/rpt_family="MER34"
repeat_region	repeat_region	complement(5963..6275)
repeat_region	repeat_region	/rpt_family="AluSp"
repeat_region	repeat_region	complement(6411..6494)
repeat_region	repeat_region	/rpt_family="MER5A"
repeat_region	repeat_region	6830..7013
repeat_region	repeat_region	/rpt_family="MLT1C"
repeat_region	repeat_region	7014..7318
repeat_region	repeat_region	/rpt_family="AluYb8"
repeat_region	repeat_region	7319..7581
repeat_region	repeat_region	/rpt_family="MLT1C"
repeat_region	repeat_region	7721..8032
repeat_region	repeat_region	/rpt_family="AluYb"
repeat_region	repeat_region	8039..8333
repeat_region	repeat_region	/rpt_family="AluSg"
repeat_region	repeat_region	9431..9460
repeat_region	repeat_region	/rpt_family="AT_rich"
repeat_region	repeat_region	9662..9829
repeat_region	repeat_region	/rpt_family="MIR"
repeat_region	repeat_region	complement(11302..11728)
repeat_region	repeat_region	/rpt_family="MER39"
repeat_region	repeat_region	complement(11824..11884)
repeat_region	repeat_region	/rpt_family="LTR16C"
repeat_region	repeat_region	complement(11928..12108)
repeat_region	repeat_region	/rpt_family="LTR16C"
repeat_region	repeat_region	12453..12725
repeat_region	repeat_region	/rpt_family="AluYb"
repeat_region	repeat_region	13377..13785
repeat_region	repeat_region	/rpt_family="MSTB"
repeat_region	repeat_region	14118..14153
repeat_region	repeat_region	/rpt_family="(CA)n"
repeat_region	repeat_region	complement(15320..15620)
repeat_region	repeat_region	/rpt_family="AluJo"
repeat_region	repeat_region	15683..15759
repeat_region	repeat_region	/rpt_family="(CA)n"
repeat_region	repeat_region	complement(15838..15893)
repeat_region	repeat_region	/rpt_family="MER91A"
repeat_region	repeat_region	complement(15915..16080)
repeat_region	repeat_region	/rpt_family="MER91A"
repeat_region	repeat_region	complement(16474..16544)
repeat_region	repeat_region	/rpt_family="L2"
repeat_region	repeat_region	17907..17920
repeat_region	repeat_region	/rpt_family="LIME"
repeat_region	repeat_region	18271..18311
repeat_region	repeat_region	/rpt_family="L2"
repeat_region	repeat_region	complement(18368..18529)
repeat_region	repeat_region	/rpt_family="AluYb"
repeat_region	repeat_region	complement(18530..18560)
repeat_region	repeat_region	/rpt_family="(CA)n"
repeat_region	repeat_region	complement(18561..18681)
repeat_region	repeat_region	/rpt_family="AluYb"
repeat_region	repeat_region	18760..19065
repeat_region	repeat_region	/rpt_family="AluSg"
repeat_region	repeat_region	complement(19638..19896)
repeat_region	repeat_region	/rpt_family="MIR"
repeat_region	repeat_region	complement(19971..20260)
repeat_region	repeat_region	/rpt_family="LIME3A"
repeat_region	repeat_region	20263..20552
repeat_region	repeat_region	/rpt_family="MER58B"
repeat_region	repeat_region	complement(20553..20816)
repeat_region	repeat_region	/rpt_family="LIME3A"
repeat_region	repeat_region	complement(20821..21069)
repeat_region	repeat_region	/rpt_family="LIM4"
repeat_region	repeat_region	complement(21071..21100)
repeat_region	repeat_region	/rpt_family="(TAAA)n"
repeat_region	repeat_region	complement(21101..21338)
repeat_region	repeat_region	/rpt_family="AluSx"
repeat_region	repeat_region	complement(21348..21598)
repeat_region	repeat_region	/rpt_family="LIM4"
repeat_region	repeat_region	21799..22104
repeat_region	repeat_region	/rpt_family="AluJo"
repeat_region	repeat_region	22151..22562

[illegible]

```

TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
    source
        /db_xref="taxon:9606"
        /clone="R26634"
        /chromosome="19"
        /map="19p13.3 between CDC34 and D19S342"
        /cell_line="5HL2-B"
        /clone_lib="LL19NC03 R chromosome 19-specific cosmid library"
        /note="Cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."
        46. .152
        /notes="DOS similarity to overlapping ESTs:--(46. .152)
        AA431731 zw77g03.s1 Soares testis NHT Homo sapiens CDNA
        clone 782260 3'; (391. .340); 100% identity.--(111. .152)
        AA609572 af15c02.s1 Soares testis NHT Homo sapiens CDNA
        clone 1031714 3'; (372. .331); 100% identity."
        complement(273. .608)
        /note="DOS similarity to overlapping ESTs:--(608. .273)
        T05239 EST03128 Homo sapiens CDNA clone HFBC75. .Score:
        621 Identity: 325/337 (96%).--(718. .308) AA496009
        zw72a03.s1 Soares total fetus Nb2HF8 9w Homo sapiens CDNA
        clone 759148 3'; Score: 755 Identity: 398/408 (97%)."
        378. .707
        /note="DOS similarity to overlapping ESTs:--AA431731
        zw77g03.s1 Soares testis NHT Homo sapiens CDNA clone
        782260 3'; (339. .11); 99% identity.--AA609572 af15c02.s1
        Soares testis NHT Homo sapiens CDNA clone 1031714 3';
        (330. .5); 99% identity.--AA448181 zw83c05.s1 Soares testis
        NHT Homo sapiens CDNA clone 782792 3'; (336. .4); 99%
        identity.--"
        <378. .468
        /note="Hypothetical human protein with no significant
        similarity to known proteins"
        /codon_start=2
        /evidence=not_experimental
        /product="R26650.2, partial CDS"
        /protein_id="AAC34213.1"
        /db_xref="PID:g3478640"
        /db_xref="GI:3478640"
        /translation="LVSPALRCLEPPHLANTLEDAAECLKQH"
        1771. .3383
        /note="DOS similarity to overlapping ESTs:--(3391. .3154)
        AA630776 ac14c10.s1 Stratagene HeLa cell s3 937218 Homo
        sapiens CDNA clone 856434 3' similar to TR:G163328 G163328
        LEUKEMIA VIRUS CELL RECEPTOR.'; (262. .1); 99%
        identity.--(1771. .2449) AA167736 zq40d04.s1 Stratagene hNT
        neuron (#937233) Homo sapiens CDNA clone 632167 3'; Score:
        1207 Identity: 655/674 (97%).--(2109. .2638) AA843415
        ak07f04.s1 Soares parathyroid tumor NBHPA Homo sapiens
        CDNA clone IMAGE:1405279 3'; Score: 969 Identity: 516/547
        (94%).--(2814. .2510) AA3364678 EST75336 pineal gland II
        Homo sapiens CDNA 5' end; Score: 582 Identity: 301/305
        (98%).--(3200. .2766) H73348 yu02f02.r1 Homo sapiens CDNA
        clone 232635 5'. Score: 717 Identity: 413/446
        (92%).--(3358. .2857) H28923 ym33c10.r1 Homo sapiens CDNA
        clone 49674 5'. Score: 756 Identity: 465/518
    
```